

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/852,020

1819 #9
7/29/98
SDF
DATE: 12/10/97
TIME: 13:07:05

INPUT SET: S22008.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

(1) General Information:

(i) APPLICANT: Maruyama, Ichiro
Maruyama, Hiroko
Brenner, Sydney

(ii) TITLE OF INVENTION: LAMBDROID BACTERIOPHAGE VECTORS FOR
EXPRESSION OF FOREIGN PROTEINS

(iii) NUMBER OF SEQUENCES: 15

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: The Scripps Research Institute, Office of
Patent Counsel
(B) STREET: 10666 North Torrey Pines Road, TPC8
(C) CITY: La Jolla
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 92037

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/852,020
(B) FILING DATE: 06-MAY-1997
(C) CLASSIFICATION: 435

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/286,888
(B) FILING DATE: 05-AUG-1994

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Fitting, Thomas
(B) REGISTRATION NUMBER: 34,163
(C) REFERENCE/DOCKET NUMBER: TSRI 432.0

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 619-554-2937
(B) TELEFAX: 619-554-6312

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Pro Val Pro Asn Pro Thr Met Pro Val Lys Gly Ala Gly Thr Thr
1 5 10 15

Leu Trp Val Tyr Lys Gly Ser Gly Asp Pro Tyr Ala Asn Pro Leu Ser
20 25 30

Asp Val Asp Trp Ser Arg Leu Ala Lys Val Lys Asp Leu Thr Pro Gly
35 40 45

Glu Leu Thr Ala Glu Ser Tyr Asp Asp Ser Tyr Leu Asp Asp Glu Asp
50 55 60

Ala Asp Trp Thr Ala Thr Gly Gln Gly Gln Lys Ser Ala Gly Asp Thr
65 70 75 80

Ser Phe Thr Leu Ala Trp Met Pro Gly Glu Gln Gly Gln Gln Ala Leu
85 90 95

Leu Ala Trp Phe Asn Glu Gly Asp Thr Arg Ala Tyr Lys Ile Arg Phe
100 105 110

Pro Asn Gly Thr Val Asp Val Phe Arg Gly Trp Val Ser Ser Ile Gly
115 120 125

Lys Ala Val Thr Ala Lys Glu Val Ile Thr Arg Thr Val Lys Val Thr
130 135 140

Asn Val Gly Arg Pro Ser Met Ala Glu Asp Arg Ser Thr Val Thr Ala
145 150 155 160

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100
101
102 Ala Thr Gly Met Thr Val Thr Pro Ala Ser Thr Ser Val Val Lys Gly
103 165 170 175
104
105
106 Gln Ser Thr Thr Leu Thr Val Ala Phe Gln Pro Glu Gly Val Thr Asp
107 180 185 190
108
109
110
111 Lys Ser Phe Arg Ala Val Ser Ala Asp Lys Thr Lys Ala Thr Val Ser
112 195 200 205
113
114
115 Val Ser Gly Met Thr Ile Thr Val Asn Gly Val Ala Ala Gly Lys Val
116 210 215 220
117
118
119 Asn Ile Pro Val Val Ser Gly Asn Gly Glu Phe Ala Ala Val Ala Glu
120 225 230 235 240
121
122
123 Ile Thr Val Thr Ala Ser
124 245
125

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

AGTGTGGAGC TCTACCCTTT C

21

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

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153
154 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
155
156 CGCCTGTAAT AAGCGGCCGC AGCT 24
157
158 (2) INFORMATION FOR SEQ ID NO:4:
159
160 (i) SEQUENCE CHARACTERISTICS:
161 (A) LENGTH: 18 base pairs
162 (B) TYPE: nucleic acid
163 (C) STRANDEDNESS: single
164 (D) TOPOLOGY: linear
165
166 (ii) MOLECULE TYPE: DNA (genomic)
167
168
169
170 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
171
172 GCGGCCGCTT ATTACAGG 18
173
174 (2) INFORMATION FOR SEQ ID NO:5:
175
176 (i) SEQUENCE CHARACTERISTICS:
177 (A) LENGTH: 910 base pairs
178 (B) TYPE: nucleic acid
179 (C) STRANDEDNESS: single
180 (D) TOPOLOGY: linear
181
182 (ii) MOLECULE TYPE: DNA (genomic)
183
184
185 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
186
187 AAATGTGAGG ACGCTATGCC TGTACCAAAT CCTACAATGC CGGTGAAAGG 50
188
189 TGCCGGGACC ACCCTGTGGG TTTATAAGGG GAGCGGTGAC CCTTACGCGA 100
190
191 ATCCGCTTTC AGACGTTGAC TGGTCGCGTC TGGCAAAAGT TAAAGACCTG 150
192
193 ACGCCCGGCG AACTGACCGC TGAGTCCTAT GACGACAGCT ATCTCGATGA 200
194
195 TGAAGATGCA GACTGGACTG CGACCGGGCA GGGGCAGAAA TCTGCCGGAG 250
196
197 ATACCAGCTT CACGCTGGCG TGGATGCCCC GAGAGCAGGG GCAGCAGGCG 300
198
199 CTGCTGGCGT GGTTTAATGA AGGCGATACC CGTGCCTATA AAATCCGCTT 350
200
201 CCCGAACGGC ACGGTCGATG TGTTCCGTGG CTGGGTCAGC AGTATCGGTA 400
202
203 AGGCGGTGAC GGC GAAGGAA GTGATCACCC GCACGGTGAA AGTCACCAAT 450
204
205 GTGGGACGTC CGTCGATGGC AGAAGATCGC AGCACGGTAA CAGCGGCAAC 500

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206
207 CGGCATGACC GTGACGCCTG CCAGCACCTC GGTGGTGAAA GGGTAGAGCT 550
208
209 GGCCTGTTAG GCCCACTCCG ACCCCGACCA CTCCCACCCC GACTCCCACC 600
210
211 CCGACCCCGA CCCCAGACTCC GACCGTTGGG CCAATTGTCA CACAGGAAAC 650
212
213 AGCTATGACC ATGATTACGC CAAGCTTGCA TGCCTGCAGG TCGACTCTAG 700
214
215 AGGATCCCCG GGTACCGAGC TCGAATTCAC TGGCCGTCGT TTTACAACGT 750
216
217 CGTGA CTGGG AAAACCCTGG CGTTACCCAA CTTAATCGCC TTGCAGCACA 800
218
219 TCCCCCTTTC GCCAGCTGGC GTAATAGCGA AGAGGCCCGC ACCGATCGCC 850
220
221 CTTCCCAACA GTTGCGCAGC CTGAATGGCG AATGGCGCCT GTAATAAGCG 900
222
223 GCCGCAGCTC 910
224
225
226
227

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 177
(C) OTHER INFORMATION: /label= Xaa
/note= "Wherein Xaa is a suppressor termination
codon"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

245
246
247 Met Pro Val Pro Asn Pro Thr Met Pro Val Lys Gly Ala Gly Thr Thr
248 1 5 10 15
249
250 Leu Trp Val Tyr Lys Gly Ser Gly Asp Pro Tyr Ala Asn Pro Leu Ser
251 20 25 30
252
253 Asp Val Asp Trp Ser Arg Leu Ala Lys Val Lys Asp Leu Thr Pro Gly
254 35 40 45
255
256 Glu Leu Thr Ala Glu Ser Tyr Asp Asp Ser Tyr Leu Asp Asp Glu Asp
257 50 55 60
258

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SEQUENCE VERIFICATION REPORT
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